Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-12. (Canceled)

13. (Previously presented) A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in an OATP-C gene, the method comprising

(a) providing a nucleic acid sample from a human identified as in need of treatment with a therapeutic agent that is transported by OATP-C, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1, and

(b) testing the sample to determine the identity of the nucleotide.

14. (Previously presented) The method of claim 13, wherein the nucleic acid sample comprises a fragment of an OATP-C DNA.

15. (Currently amended) The method of claim 13, wherein the ~~human is in need of treatment with~~ therapeutic agent is a statin.

16. (Currently amended) The method of claim 13, wherein the ~~human is in need of treatment with~~ therapeutic agent is a xenobiotic.

17. (Previously presented) The method of claim 13, wherein step (b) comprises performing a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

18. (Previously presented) The method of claim 13, wherein the nucleotide is a C.

19. (Previously presented) The method of claim 13, wherein the nucleotide is not a G.

20. (Previously presented) The method of claim 13, wherein the nucleotide is in a codon that does not encode a glycine.

21. (Previously presented) The method of claim 13, wherein the nucleotide is in a codon that encodes an arginine.

22. (Currently amended) A method for determining the presence or absence of a ~~single nucleotide polymorphism (SNP)~~ SNP in an OATP-C gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as having or at risk for developing an OATP-C-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1; and

(b) testing the sample to determine the identity of the nucleotide.

23. (Currently amended) The method of claim 22, wherein the ~~human has or is at risk for developing~~ OATP-C-mediated disease is hyperlipoproteinemia.

24. (Currently amended) The method of claim 22, wherein the ~~human has or is at risk for developing~~ OATP-C-mediated disease is cardiovascular disease.

25. (Previously presented) A method for determining the presence or absence of a SNP in an OATP-C gene, the method comprising

(a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1; and

(b) determining the identity of the nucleotide by using a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

26. (Previously presented) A method for determining the presence or absence of a SNP in an OATP-C gene of a human, the method comprising

(a) providing a fragment of an OATP-C nucleic acid from the human, wherein the fragment comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO:1; and

(b) determining the identity of the nucleotide by using a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

27. (Currently amended) A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that ~~the~~ a nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is a C.

28. (Currently amended) A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that ~~the~~ a nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is not a G.

29. (Currently amended) A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that ~~the~~ a nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is in a codon that does not encode a glycine.

30. (Currently amended) A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that ~~the~~ a nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is in a codon that encodes an arginine.

31. (Previously presented) A method to assess the pharmacogenetics of a drug, the method comprising

(a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1;

(b) determining the identity of the nucleotide; and

(c) correlating (i) the identity of the nucleotide to (ii) the human's response following administration of the drug, thereby assessing the pharmacogenetics of the drug.

32. (Previously presented) A method for determining the presence or absence of at least one SNP in an OATP-C gene, the method comprising

(a) providing a nucleic acid sample from a human, wherein the sample comprises nucleotides at positions corresponding to

positions 510, 696, 1299, 1312, 1347, 1561, 2028, 2327, and 2342 of SEQ ID NO:1,

positions 321 and 1332 of SEQ ID NO:3,

position 41 of SEQ ID NO:4,

positions 109 and 244 of SEQ ID NO:5,

positions 117 and 283 of SEQ ID NO:6,

positions 209 and 211 of SEQ ID NO:7,

positions 63 through 68 of SEQ ID NO:8,

position 53 of SEQ ID NO:9,

position 75 of SEQ ID NO:10,

position 162 of SEQ ID NO:11, and

position 84 of SEQ ID NO:12; and

(b) determining the identity of at least one of the nucleotides by a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

33. (Previously presented) The method of claim 32, wherein the identities of all 28 of the nucleotides are determined.

34. (Previously presented) A method of treatment comprising:

(a) identifying a patient in need of treatment with a therapeutic agent that is transported by OATP-C;

(b) determining whether the patient has a glycine at the amino acid position of OATP-C corresponding to position 488 of SEQ ID NO:2; and

(c) prescribing an appropriate dosage of the therapeutic agent.

35. (Currently amended) A method of treatment comprising:

(a) identifying a patient having or at risk for developing an OATP-C-mediated disease;

(b) determining whether the patient has a glycine at the amino acid position of OATP-C corresponding to position 488 of SEQ ID NO:2; and

(c) prescribing an appropriate dosage of ~~the~~ a therapeutic agent.

36. (Previously presented) The method of claim 35, wherein step (b) comprises:

(i) providing a nucleic acid sample from the patient, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1; and

(ii) determining the identity of the nucleotide by use of a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

37. (Currently amended) The method of claim 35, wherein the patient is determined not to ~~comprising determining that the patient does not~~ have a glycine at the amino acid position of an OATP-C polypeptide corresponding to position 488 of SEQ ID NO:2.

38. (Currently amended) The method of claim 35, wherein the patient is determined to have ~~comprising determining that the patient has~~ an arginine at the amino acid position of an OATP-C polypeptide corresponding to position 488 of SEQ ID NO:2.

39. (Previously presented) An isolated nucleic acid encoding a protein comprising the amino acid sequence of SEQ ID NO:2, wherein the amino acid at the position corresponding to position 488 of SEQ ID NO:2 is not glycine.

40. (Previously presented) An isolated nucleic acid comprising SEQ ID NO:1, wherein the nucleotide of the nucleic acid at the position corresponding to position 1561 of SEQ ID NO:1 is a C.

41. (Previously presented) An isolated nucleic acid that hybridizes under stringent conditions with a probe consisting of the nucleotide sequence of SEQ ID NO:1 or the complement thereof, wherein the nucleotide of the probe at the position corresponding to position 1561 of SEQ ID NO:1 is a C.

42. (Previously presented) A polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the amino acid corresponding to position 488 of SEQ ID NO:2 is not glycine.

43. (Previously presented) A polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2 at least 10 amino acids in length, wherein the polypeptide comprises an amino acid corresponding to position 488 of SEQ ID NO:2 and that amino acid is not a glycine.

44. (Previously presented) An antibody that binds to human OATP-C when the amino acid corresponding to position 488 of SEQ ID NO:2 is arginine, but not when the amino acid at position 488 is glycine.

45. (Currently amended) A method of performing a linkage study, the method comprising

(a) providing a nucleic acid sample from each of two or more humans identified as having or at risk for having an OATP-C-mediated disease, wherein ~~the~~ each sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO:1;

(b) testing each sample to determine the identity of the nucleotide; and

(c) comparing (i) the frequency with which a C occurs at the position corresponding to position 1561 of SEQ ID NO:1 in the samples, with (ii) the frequency with

which C occurs at the position corresponding to position 1561 of SEQ ID NO:1 in nucleic acid samples from the population at large.

46. (New) A method for determining the presence or absence of a SNP in an OATP-C gene, the method comprising

(a) providing a nucleic acid sample from a human identified as having or at risk for developing an OATP-C-mediated disease, wherein the sample comprises nucleotides at each of the following positions:

positions 510, 696, 1299, 1312, 1347, 1561, 2028, 2327, and 2342 of SEQ ID NO:1,

positions 321 and 1332 of SEQ ID NO:3,

position 41 of SEQ ID NO:4,

positions 109 and 244 of SEQ ID NO:5,

positions 117 and 283 of SEQ ID NO:6,

positions 209 and 211 of SEQ ID NO:7,

positions 63 through 68 of SEQ ID NO:8,

position 53 of SEQ ID NO:9,

position 75 of SEQ ID NO:10,

position 162 of SEQ ID NO:11, and

position 84 of SEQ ID NO:12; and

(b) testing the sample to determine the identity of all 24 nucleotides.